Gerald Amiel Ballena

• Metro Manila, Philippines

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Professional Summary

Bioinformatics specialist with extensive experience in developing scalable workflows for high-throughput sequencing data, single-cell analysis, and visualization tools. Proven expertise in automating data pipelines, ensuring reproducibility, and delivering actionable results for public health and environmental research.

Experience

Project Technical Specialist (Contract)

University of the Philippines, College of Public Health

2024 - Present

- Designed scalable metagenomics pipelines for microbial community profiling, integrating tools like Kraken2, Bracken, and scikit-bio.
- Automated preprocessing and trimming workflows using Snakemake, enhancing reproducibility and reducing manual effort by 90%.
- Developed modular workflows for taxonomic profiling, diversity analysis, and functional annotation.
- Visualized complex biological datasets using tools like **ggplot2**, **Plotly**, and **Shiny**.
- Collaborated with multidisciplinary teams to analyze high-dimensional sequencing data and present findings for research publications.

Key Projects

- Single-Cell Workflow Development: Designed Python and R pipelines for preprocessing, integration, and visualization of single-cell datasets.
- K-mer and Shannon Entropy Analysis: Quantified sequence complexity using entropy metrics for diversity assessment across datasets.
- Metagenomic Workflow Automation: Built Snakemake pipelines for reproducible analysis of multi-terabyte sequencing datasets.

Certifications

• AI Fundamentals	2024
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Education

University of the Philippines Diliman

Graduated: July 2022

Thesis: In silico assessment of the association of pathogenicity and metal-resistance potential of Fusarium spp. . Preprint Link

Accomplishments: DOST ASTHRDP-Scholarship

University of the Philippines Baguio

Graduated: June 2018

Thesis: Bioelectrocatalysis by Novel Electrogenic Alkaliphilic Bacteria Bacillus sp. BAB-3442 Using Dual-Chambered

\mathbf{Skills}

Programming

Python, R, Bash

Bioinformatics Tools

• Single-Cell Analysis: scikit-learn

• Metagenomics: Kraken2, MetaPhlAn, HUMAnN

• Assembly and Binning: MEGAHIT, MetaWRAP, CheckM

• Annotation: Prokka, EggNOG-mapper, KEGG

• Quality Control: FastQC, Trimmomatic, Cutadapt, BUSCO

• Phylogenetics: RAxML, FastTree, IQ-TREE

Data Analysis & Visualization

• Visualization: ggplot2, Plotly, Shiny, matplotlib

• Machine Learning: scikit-learn, caret (R)

Technical Skills

• Version Control: Git, GitHub

• Workflow Automation: Snakemake, Conda, YAML

• Virtualization: Docker, WSL2

• Cloud Computing: AWS, GCP (Familiarity)

References

Available upon request and if shortlisted.